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Thermus thermophil
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H. pylori cytoplas
Staphylococcus aur
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Human polypeptide
Novel human diagno
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27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
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Yamamoto RT,
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and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The artisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                           81;
                                                                                                                                                                                                              Length
                                                                                                                                                                                                           41.1%; Score 1666.5; DB 22; Lengtl
48.7%; Pred. No. 2.3e-139;
Artive 92; Mismatches 198; Indels
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Best Local Similarity
Matches 352; Conserv
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AAU33631 standard; Protein; 474 AA.

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                                                                                                                                                                                   genes, their use in the discovery of novel antibiotics, the essential CC genes themselves and the encoded proteins. The prokaryotes used are Escherichia coll, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The convention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, CC and to obtain antibodies capable of binding to the expressed proteins, CC The proteins can be used to screen compounds in rational drug discovery CC programmes. The antisense nucleic acid sequence is also useful to screen CC wide variety of organisms. The present sequence represents an CC a wide variety of organisms. The present sequence represents an CC Note: The sequence data for this patent did not form part CC format directly from WIPO at CC format directly from WIPO at CC format directly fublished_pct_sequences.
                                                                                                                       Query Match
Best Local (
                                                                                                          Matches
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23-OCT-2000;
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22-DEC-2000;
                                                                                                                                                                Sequence
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)B; AAS51490.
                                                   HNVPTTSRKALKDIASFIKEDDSRTQCVTLEENVKEFGVTYFGLSDKRQGIVHVIGPEQG 128
HNVPTTRTERKGGIAA-IADEVSRLQVQTLDENCDDFGITEFKMNDVRQGIVHVVGPEQG
                                                                                                                         Similarity
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; antibacterial; drug design.
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2000US-242578P.
2000US-253625P.
2000US-257931P.
                                                                                                            Conservative
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                                                                                                         ; Score 1507.5; DB 22; Pred. No. 2.1e-125; 61; Mismatches 113;
                                                                                                                                     DB 22; Length 474;
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23-OCT-2000;
27-NOV-2000;
The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
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                                                                                                     New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
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23-MAY-2000;
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                                                                                                                                          N-PSDB;
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Yamamoto RT,
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16-FEB-2001;
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; 2000US-207727P.
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for antibiotic development. The antiense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antiense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fitp.wipo.int/pub/published_pct_sequences.
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62.1%; Pred. No. 6.6e-123;
ive 59; Mismatches 111; Indels
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Matches 293; Conservative
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The invention relates to antieense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential comes themselves and the encoded proteins. The prokaryotes used are genes themselves and the encoded proteins, almonella typhi, Klebsiella prediction is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen corrections in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                                                                                                                                                                                                 Trawick JD,
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                                                                                                                                                                                                                                                               Wall
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                                                                                                                                                                                                                                                               Zyskind JW,
                                              2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
2001US-269308P.
  2000US-191078P.
2000US-206848P.
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Best Local Similarity 59.4%
Matches 281; Conservative
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                                                                                                                                                                                                           (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                               Ohlsen I
Xu HH;
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21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
                                                                                                                            22-DEC-2000;
16-FEB-2001;
                                                                         23-OCT-2000;
27-NOV-2000;
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Yamamoto RT,
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RESULT 5
AAU38424
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                                        The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the CC genes, their use in the discovery of novel antibiotics, the essential CC genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The CC invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used CC to identify proteins used in proliferation, to express these proteins, CC and to obtain antibodies capable of binding to the expressed proteins. CC The proteins can be used to screen compounds in rational drug discovery CC programmes. The antisense nucleic acid sequence is also useful to screen CC for homologous nucleic acids which are required for cell proliferation in CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this pattent did not form part of the printed specification, but was obtained in electronic CC format directly from WIPO at
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26-MAY-2000; 2000US-207727P.

23-OCT-2000; 2000US-242578P.

27-NOV-2000; 2000US-253625P.

22-DEC-2000; 2000US-257911P.

16-FEB-2001; 2001US-269308P.
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23-MAY-2000;
26-MAY-2000;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids - \,
                                                                                                                                                                                                                                                                                                                                                        Example 3; Seq ID No 14017; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haselbeck R,
Yamamoto RT,
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                            ttp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ELIT-) ELITRA PHARM INC.
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DB; AAS56283.
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466 AA;
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Xu HH;
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Query Match

S . 88

Score 1450.5;

DB

22;

Length 466;

Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene

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RESULT 6
AAG91198
ID AAG9
XX AAG9
XX AAG9
XX Cory
XW Cory
XW Cory
XW Cory
XW Cory
YW EP11
PD 20---
YX 18---
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07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                  Nakagawa
Tateishi
                                                                                                                       WPI; 2001-376931/40.
N-PSDB; AAH66417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Coryneform bacterium; amino organic acid synthesis.
                                                                                                                                                                                                                                                                        (KYOW ) KYOWA HAKKO KOGYO KK.
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Senoh A, Ikeda M, Ozaki A;
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3; Mismatches 114;
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9
                            The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitumins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.2%; Score 1347.5; DB 22; Length 481; 57.6%; Pred. No. 4.1e-111; ative 61; Mismatches 127; Indels 13;
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           Claim 17; SEQ ID NO: 4952; 246pp + Sequence Listing; English.
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Matches 273; Conservative
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99DE-1041380. 99DE-1041394. 99DE-1041396. 99DE-1042076.

99DE-1040832. 99DE-1041378. 99DE-1041379.

99DE-1042087. 99DE-1042088. 99DE-1042095.

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Haberhauer G;

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                                                                                                      Corynebacterium glutamicum; metabolic pathway protein; MP protein; fine chemical production; microorganism; organic acid; nucleoside; nonproteinogenic amino acid; purine base; pyrimidine base; nucleot lipid; saturated fatty acid; diad; vitamin carbohydrate; aromatic compound; cofactor; polyketide; enzyme.
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27-AUG-1999;
Nucleic acids from Corynebacterium glutamicum encoding metabolic pathway proteins, useful for producing fine chemicals in
                        WPI; 2001-137957/14.
N-PSDB; AAF71886.
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                                             AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum MP nucleic acids are useful for the production of fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides and enzymes.
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  nonproteinogenic amino acids
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  microorganisms, including organic acids, and purine and pyrimidine bases -
                              Claim 20; Page 549-551; 1737pp; English
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Matches 264;
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ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to sorreen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240
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                                                                                                                                                                                                         Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
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54.7%; Pred. No. 6.6e-107;
tive 69; Mismatches 125;
                                                                                                                                                                                                                                                                              Disclosure; SEQ ID 3892; 267pp; English.
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97US-055779P.
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N-PSDB; ABN91592.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Bscherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets invention to development. The antisense nucleic acids can also be used to identify protein the content of the process of the content of the c
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23-OCT-2000;
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23-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAR-2001; 2001WO-US09180
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nes 257; Conserv
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                                                                                                                                                                                                         QTLFDKVWNRHVLYGKLGEPQLLYIDLHLIHEVTSPQAFEGLRLQNRKLRRPDLTFATLD
                                                                                                                                                                                                                                                           QTLYDKVLQAHVVDEKLDGTVLLYIDRHLVHEVTSPQAFEGLRNAGRKVRRPDCTLATTD
LTQPGKTIVCGDSHTATHGAFGAIAFGIGTSEVEHVFATQTLWQTKPKNLKIDINGTLPT 175
                                              FTLPGTTVVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNMRIQVDGELAP
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                                                                                                                                                                                                                                                                                                                                                                                                                         456 AA;
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2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
2001US-269308P.
                                                                                                                                                                                                                                                                                                             31.6%; Score 1282; DB 22; ilarity 54.4%; Pred. No. 2.6e-105; Conservative 64; Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comprise sequences of antisense nucleic
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                                                                                           DIFN-IKDEIANKQITTLQKNAIDFGVHIFDMGSDEQGIVHMVGPETG
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                                                                                                                                                                                                                                                                                                                  Indels
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23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins.
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                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
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N-PSDB; AAS55194.
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Yamamoto RT,
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2000US-242578P.
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Xu HH;
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The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WiPO at frow wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibacterial, gene therapy, vaccine, biosynthesis, biodegradation, vitamin B12; bacterial infection, disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DITFEYVKGRPFADNF----AKSVDKWRELYSDDDAIFDRVIELDVSTLEPQVTWGTNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EDVVPITGVVPDPETFATEAKKADGRRMLQYMGLKAGTPMEDI PVDKVFIGSCTNSRIED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LRAAAAVVKGRKKAPNVKSAMVVPGSGLVKTQAEEEGLDKIFEEAGFEWREAGCSMCLGM
                                                                                                                                                                                                                      9 QTLYDKVLQAHVVDEKLDGTVLLYIDRHLVHEVTSPQAFEGLRNAGRKVRRPDCTLATTD
                                                                                                                                                                                                                                    3 QTLFDKVWNRHVLYGKLGEPQLLYIDLHLIHEVTSPQAFEGLRLQNRKLRRPDLTFATLD
                                                                                                                                                                                                                                                                                                                                                                                  GVSSKDVVLHAIGIIGTAGGTGAVIEFCGSVIRSLSMEARMSICNMSIEGGARAGMVAPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    480
                                                                                                                                                                   Length 456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NPDILAPQERCASTSNRNFEGROGAGGRTHLMSPVMAAAAGIVGKLADVRKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                31.6%; Score 1282; DB 22;
54.4%; Pred. No. 2.6e-105;
iive 64; Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               monocytogenes protein #876.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB48172 standard; Protein; 462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-APR-2001; 2001WO-FR01118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                   Best Local Similarity 54.41
Matches 257; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Listeria monocytogenes
                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                           456 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200177335-A2.
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                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                129
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ABB48172
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The present invention relates to the genome sequence of Listeria

monocytogenes EGD-e (see ABA01041). The genome sequence and fragments of
the are useful for selecting probes and primers for detecting genes in L.
monocytogenes and related organisms, and for studying genetic
monocytogenes and related organisms, and for studying genetic
polymorphisms and other genomes. The present sequence is a protein
expressed from the genome sequence of the present invention. Proteins
cypressed from the genome sequence are useful for raising specific
antibodies, identification of L. monocytogenes and related organisms, and
correcting compounds that regulate gene expression and cell replication
EB12. The genome sequence and proteins encoded by it are also useful for
selecting compounds that regulate gene expression and cell replication
condition. In monocytogenes-related diseases. In addition, the genome
sequence and proteins encoded by it are useful in pharmaceutical and
vaccines compositions for the treatment or prevention of infections by L.
concorpogenes and related organisms.
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       Buchrieser C, Frangeul L, Couve B, Rusniok C, Fsihi H, Dehoux P, Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart F Daniels J, Goebel W, Kreft J, Kuhn M, Ng B, Vazquez-Boland JA; Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A; Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L; Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HNVPTTSRKALKDIASFIKEDDSRTQCVTLEENVKEFGVTYFGLSDKRQGIVHVIGPEQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVSSKDVVLHAIGIIGTAGGTGAVIEFCGSVIRSLSMEARMSICNMSIEGGARAGMVAPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EITFEYLKGRPLAPKYDSPEWHKATQYWKNLQSDPGAKYDIDVFIDAKDIVPTLTWGTSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31.6%; Score 1279.5; DB 23; Length 462; 53.8%; Pred. No. 4.5e-105;
                                                                                                                                                                                                                                                                      for Listeria monocytogenes, useful e.g. for Listeria and related bacterial infections,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 4.5e-105;
; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                 Claim 6; SEQ ID No 877; 192pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65;
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                                                                                                                                                                                                                                                                        Genomic sequence for
and prevention of Lis
related polypeptides
                                                                                                                                                                                                                           WPI; 2002-010914/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           462 AA;
                                                                                                                                                                                  Voss H;
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Matches 254;
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LRAAAAVVKGRKKAPNVKSAMVVPGSGLVKTQAEEEGLDKIFEEAGFEWREAGCSMCLGM 428

NPDILAPQERCASTSNRNFEGRQGAGGRTHLMSPVMAAAAGIVGKLADVRKL 480

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292 369 345

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404 NPDQVPDGVHCASTSNRNFEGRQGKGARTHLVSPAMAAAAAINGHFIDIRKV 455

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RESULT 13
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Matches
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                                                                                                                                                                                                                                                                         The genes involved in the pathway for synthesis of branched ami acids in L.lactis subsp. lactis are organised in two units containing the leu (including leuc) and ilv genes, respectively Both units are necessary for the synthesis of leucine but only second unit is required for synthesis of Ile and Val. The ilvB and ilvN genes and the subunits of alpha-acetolactate synthase that they code for are claimed.
                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig
                                                                                                                                                                                                                                                                                                                                                                                                   DNA coding for alpha-aceto:lactate synthase - for enhancing di:acetyl prodn. in microorganisms, esp. for mfr. of dairy prods.
                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAQ64211
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1994-128287/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ehrlich S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FR2696190-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lactococcus lactis (subsp. lactis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L.lactis branched amino acid synthesis leuC
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                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INRG ) INRA INST NAT RECH AGRONOMIQUE (AGRI-) AGRIC & FOOD RES COUNCIL.
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177
                       189
                                                117
                                                                                                                                                                                                           Local
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                                                                                                                                              QTLYDKVLQAHVVDEKLDGTVLLYIDRHLVHEVTSPQAFEGLRNAGRKVRRPDCTLATTD
                                                                                               HNVPTQNIFNIQDLI-----SKKQIDTFTKNVKEFDVPAETHGGKGQGIVHMVAPESG
                                                                                                             HNVPTTSRKALKDIASFIKEDDSRTQCVTLEENVKEFGVTYFGLSDKRQGIVHVIGPEQG
GIYSKDFILALIAKYGVDAGVGYAVEYSGDAISDLSMEERMTICNMSIEFGAKIGLMNPD
                      GVSSKDVVLHAIGIIGTAGGTGAVIEFCGSVIRSLSMEARMSICNMSIEGGARAGMVAPD
                                               RTQPGKTIVCGDSHTATNGAFGAIAFGIGTSEVEHVLATQTIWQVKPKRMKIEFQGHPQK 176
                                                                      FTLPGTTVVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNMRIQVDGELAP
                                                                                                                                                                                                al Similarity
240; Conserv
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nilarity 50.4%;
Conservative 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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436
/note= "Val residue
                                                                                                                                                                                                                                                                                                                                                                           2; 45pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Val residue corresponds to CTG codon"
                                                                                                                                                                                                 61;
                                                                                                                                                                                                Score 1138.5; DB
Pred. No. 1.7e-92;
1; Mismatches 154
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                                                                                                                                                                                                 154;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product
                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                           wo units, respectively.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              valine;
food flavouring;
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                                                                                                                                                                                                                                                                                                                                                    amino
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RESULT 14
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                                                                    Query Match
Best Local
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                                                                                                                                                                The present invention is related to a Lactococcus lactis nucleotide sequence (ABA,90521) and related proteins (ABB3300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese.

Note: The sequence data for this patent is based on equivalent rates.
                                                                                                                                                                                                                                                                                                                                   New nucleotide sequence useful in lactis and related species -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB54552;
                                                                                                           Sequence
                                                                                                                                    Note: The sequence data for this patent is based on equivalent patent WO200177334 (published 18-OCT-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                        Claim 6; SEQ ID No 1254; 2504pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                        Bolotine A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-APR-2000; 2000FR-0004630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biosynthesis; biodegradation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB54552 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lactococcus lactis protein leuC
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                                                                                                                                                                                                                                                                                                                                                                                                                                   (INRG ) INRA INST NAT RECH AGRONOMIQUE
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                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MNPDQIPEYVHCASTSNRNFEGROGHNARTHVCSPAMAAAAAIAGKFVDVRMLVTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MNPDILAPQERCASTSNRNFEGRQGAGGRTHLMSPVMAAAAGIVGKLADVRKL-TD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DLRAAAAVVKGRKKAPNVKSAMVVPGSGLVKTQAEEEGLDKIFEEAGFEWREAGCSMCLG 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----GMGLEFGEKFPEINNDLNYERAYQYMDLKPGQTASDIDLGYIFIGSCTNARLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKTYDYVKGREHAPK----NFDEAVSKWEKLVSDSDAQYDKILSLDVSQLKPMVTWGTNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EITFEYLKGRPLAPKYDSPEWHKATQYWKNLQSDPGAKYDIDVFIDAKDIVPTLTWGTSP 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DLEEAAKIIGDRHIADGL-TGIVVPGSRPVKEAAEAQGLDKIFKEAGFEWREPGCSACLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDVVPITGV-VPDPETFATEAKKADGRRMLQYMGLKAGTPMEDIPVDKVFIGSCTNSRIE 367
                       QTLYDKVLQAHVVDEKLDGTVLLYIDRHLVHEVTSPQAFEGLRNAGRKVRRPDCTLATTD
                                                                                                                                                                                                                                                                                                                                                                                2002-043418/06
 240;
                                                                                                             460 AA;
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                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          Sorokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000FR-0004630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein;
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                                                                  27.9%;
                                                                                                                                                                                                                                                                                                                                                                                                        A,
                                                                                                                                                                                                                                                                                                                                                                                                          Renault P,
                                                     59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      460
                                                                  Score 1132.5;
Pred. No. 5.86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lactic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                    the identification or Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bacterium; yogurt; cheese.
                                                                                                                                                                                                                                                                                                                                                                                                           Ehrlich
                                                     .5; DB 23;
5.8e-92;
nes 156; I
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                                                       Indels
                                                                                 Length
                                                       21;
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                                                     Gaps
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Staphylococcus aureus protein, immune response induction, eye infection, antibody production; T-cell immune response; gastrointestinal infection, respiratory infection; inhibitor; bacterial infection; cardiac infection, central nervous system; kidney infection; urinary tract infection, antimicrobial compound identification; broad spectrum antibiotic;
                                                 188
                                                              248
                                                                                                                308
                                                                                                                                                                                                                      |::||||||:||:||------GMGLEFGEKFPEINNDLNYERAYQYMDLKPGQTASAIDLGYIFIGSCTNARLG 345
                                                                                                                                                                            237 EKTYDYVKGREHAPK----NFDEAVSKWEKLVSDSDAQYDKILSLDVSQLKPMVTWGTNP 292
                                                                                                                                                                                                                                                                                404
                                                                                                                                                                                                        EDVVPITGV-VPDPETFATEAKKADGRRMLQYMGLKAGTPMEDIPVDKVFIGSCTNSRIE 367
                                                                                                                                                                                                                                                        DLRAAAAVVKGRKKAPNVKSAMVVPGSGLVKTQAEEEGLDKIFEEAGFEWREAGCSMCLG 427
            64 HNVPTQDIFNIQDLI-----SKKQIDTFTKNVKEFDVPAETHGGKGQGIVHNVAPESG
                                                                                                                                                                                                                                                                      HNVPTTSRKALKDIASFIKEDDSRTQCVTLEENVKEFGVTYFGLSDKRQGIVHVIGPEQG
                                                 FTLPGTTVVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNMRIQVDGELAP
                                                                                                  GVSSKDVVLHAIGIIGTAGGTGAVIEFCGSVIRSLSMEARMSICNMSIEGGARAGMVAPD
                                                                                                                                                     EITFEYLKGRPLAPKYDSPEWHKATQYWKNLQSDPGAKYDIDVFIDAKDIVPTLTWGTSP
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MNPDQIPEYVHCASTSNRNFEGRQGHNARTHLCSPAMAAAAAIAGKFVDVRTLVTD 460
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                                                                                                                                                                                                                                                                                                         MNPDILAPQERCASTSNRNFEGRQGAGGRTHLMSPVMAAAAGIVGKLADVRKL-TD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid sequences from Staphylococcus aureus WCHU29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoded by TNC
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RW,
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Reichard B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3-Isopropylmalate dehydratase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hodgson JE,
, Pratt JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "unspecified,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "unspecified,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                AAW77717 standard; Protein; 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97EP-0307485
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Nicholas RO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAV53507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Black MT, Bur
~++o MA,
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Ward JM;
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This sequence represents a Staphylococcus aureus protein, that based on homology with a Lactococcus lactis subsplactis (Streptococcus lactis) brotein, is a 3-isopropylmalate dehydratase (Ec 4.2.1.33) (isopropylmalate isomerase) (Alpha-Ipm isomerase) (Ipmi), and is encoded by a DNA sequence of the invention.

The DNA sequences were isolated from Staphylococcus aureus WCHU29 (NCIMB 40771). Host cells containing the DNA sequences are used to produce polypeptides or fragments. The proteins are used in the treatment of disease, for inducing an immune response by administering them, to produce antibody and/or T-cell immune response. Antagoniste of the proteins are used for the inhibition of bacterial polypeptides.

Conditions which may be treated include bacterial infections, especially using tract, skin, bones and joints. The proteins can also be used to identify antimicrobial compounds which are broad spectrum antibiotics, especially useful in the treatment of H. pylori infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194
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treatment of bacterial infections of e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 VLQAHVVDEKLDGTVLLYIDRHLVHEVTSPQAFEGLRNAGRKVRRPDCTLATTDHNVPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SRKALKDIASFIKEDDSRIQCVILEENVKEFGVIYFGLSDKRQGIVHVIGPEQGFILPGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TVVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNMRIQVDGELAPGVSSKD

    epidermidis open reading frame protein sequence SEQ ID NO:1042.

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                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                                                                                                                                        Length 264;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                     18.5%; Score 749; DB 19;
53.8%; Pred. No. 3.9e-58;
iive 39; Mismatches 75;
                 respiratory tract and central nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LKGRPLAPKYDSPEWHKATQYWKNLQSDPGAKY 287
                                               Claim 11; Page 348-349; 390pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :|||| : :| : :| : :|
234 VKGRPFADNF----AKSVDKWRELYSDGTTRY
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in vaccines and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus epidermidis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccination; endocarditis.
                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 53.83
Matches 147; Conservative
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                                                                                                                                                                                                                                                                                                                                                                         264 AA;
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                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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AAG81974
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. CC (II) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the CC s. epidermidis polypeptides (II) via the production of vectors (CC containing them which are used to produce hosts cells which express the CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. CC The polypeptides may also be used to assay for other inhibitors of their CC activity and therefore identify compounds that may be used for the cC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA CC polypucleotide sequences from the present invention. AAH55091 to CC AAH55098 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention. CC N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even consequences are given in the disclosure for SEQ ID NO:4465 to 4472, consequences are present for SEQ ID NO:4455 to 4464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Sim.
Matches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                   Pyrococcus abyssi
                                                     Hyperthermophilic archaeon;
                                                                                             Putative 3-isopropylmalate dehydratase/aconitase large subunit
                                                                                                                                                                         AAB96358;
                                                                                                                                                                                                             AAB96358 standard; Protein;
                                                                                                                                     29-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                              GLDKIFEEAGFEWREAGCSMCLGMNPDILAPQERCASTSNRNFEGRQGAGGRTHLMSPVM 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTPMEDIPVDKVFIGSCTNSRIEDLRAAAAVVKGRKKAPNVKSAMVVPGSGLVKTQAEEE 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AKYDIDVFIDAKDIVPTLTWGTSPEDVVPITGVVPDPETFATEAKKADGRRMLQYMGLKA 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEARMTICNMAIEAGAKYGLMQPDETTFNYVKGRPYATDFDS-----SMAWWKELYSDDD
                                                                                                                                                                                                                                                                                                                                              AAAAGIVGKLADVRKL 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AYFDKVIELDVTNLEPQVTWGTNPEMGVSFSNPFP-----EIKNANDQRAYDYMGLHP 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        245 AA;
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                                                         hyperthermophilic
                                                                                                                                                                                                               423 AA
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to the genomic sequence of Pyrococcus abyssi (see AAF86431 and AAH41223-7) and P. abyssi proteins. P. abyssi a hyperthermophilic archaeon, which is isolated from deep-sea hydrothermal vents. The present sequence is one such P. abyssi protein. The proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up 110 degrees centigrade.

Note: This patent is in the same patent family as WO200065062, which contains additional sequences as shown in AAB99132-AAB99143, AAH75903-AAH75920 and AAG66436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; Pages 1038-1040; 1657pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleotide sequences isolated proteins useful in industry -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Forterre P,
Querellou J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 TLYDKVLQAHVVDE--KLDGTVLLYIDRHLVHEVTSPQAFEGLRNAG-RKVRRPDCTLAT
                                                                                                                                                                                                                                                                                                                                                                                                                                      4
                                                                                                                                                    SPEDVVPITGVVPDPETFATEAKKADGRRMLQYMGLKAGTPMEDIPVDKVFIGSCTNSRI 366
                                                                                                                                                                                                                                               QPYVTGKDLILHTIGDIGVNGALYKVMEFSGSVIEELSVEQRWTMSNMAIEAGAKTGIIE
                                                                                                                                                                                                                                                                 APGVSSKDVVLHAIGIIGTAGGTGAVIEFCGSVIRSLSMEARMSICNMSIEGGARAGMVA 246
                                                                                                                                                                                                                                                                                                           LGLVLPGDLIIGADSHTCTYGALGAFATGVGSTDLAVAMATGEAWFRVPETMKFIYEGEL
                                                                                                                                                                                                                                                                                                                                   QGFTLPGTTVVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNMRIQVDGEL
                                                                                                                                                                                                                                                                                                                                                                        LDHFTPN-----KDI-----KSAEQCKSSREFAKEMGIKWF-FEGGSVGVEHCLLPE 109
                                                                                                                                                                                                                                                                                                                                                                                                                                    TIAEKILADHSEREEVKPGEIVMAKLDFVFGNDVTMPLAIKKFRELGVKRVFDRERIAIV 63
                                                                                                                       LPENTVPI ----
                                                                                                                                                                                                             PDEITFEYLKGRPLAPKYDSPEWHKATQYWKNLQSDPGAKYDIDVFIDAKDIVPTLTWGT
GGHMGVLASGERAVSTTNRNFVGRMGHPKSEVYLANPYVAAASAVLGRIA
                           GMNPDILAPQERCASTSNRNFEGROG-AGGRTHLMSPVMAAAAGIVGKLA
                                                           EDLRMAAEILEGQKVAKWVR-LIVIPCSPTVYWKALKEGLIEIFLEAGAVIGPPTCGPCL
                                                                                       EDLRAAAAVVKGRKKAPNVKSAMVVPGSGLVKTQAEEEGLDKIFEEAGFEWREAGCSMCL
                                                                                                                                                                                     PDKKTLDYVKER---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.7%; Score 637.5; DB 22; 35.3%; Pred. No. 7.3e-48; tive 77; Mismatches 166;
                                                                                                                         --SKAAKM-----
                                                                                                                                                                                   ----AKRKFKVYKSDEDAKYYKVIEYDVTNWEPVVAFPH
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18-JUN-1999;
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11-AUG-1999;
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03-AUG-1999;
04-AUG-1999;
04-AUG-1999;
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27-JUL-1999;
   Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                               Arabidopsis thaliana protein fragment SEQ ID NO: 35684
   AAG29924 standard; Protein; 461 AA
                                                                                                                                                                                                                                                                                                                                     9905-0123180
9908-0123548
9908-0126249
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                                                                17-OCT-2000 (first entry)
                                                                                                                                                                                            Arabidopsis thaliana
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                                  AAG29924;
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427 449 375 394 316 348 286

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Query Match
13.8%; Sco
Best Local Similarity 32.1%; Pro
Matches 164; Conservative 73;
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22-OCT 1999
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31-AUG-1999
01-SEP-1999
07-SEP-1999
   172 TKRSKNMRIQVDGELAPGVSSKDVVLHAIGIIGTAGGTGAVIEFCGSVIRSLSMEARMSI
                                                                                                                              ANPDYKGVCHVALAQEGHCRPGEVLLGTDSHTCTAGAFGQFATGIGNTDAGFVLGTGKIL
                                                                          LSDKRQGIVHVIGPEQGFTLPGTTVVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLI
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99US-0161361

99US-0161361
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06-APR-1999;
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16-APR-1999;
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25-MAR-1999;
29-MAR-1999;
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09-MAR-1999;
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99US-0121825

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99US-0160981.

28-JUL-1999; 02-MUG-1999; 02-MUG-1999; 03-MUG-1999; 04-AUG-1999; 04-AUG-1999; 04-AUG-1999; 06-AUG-1999; 07-CCT-1999; 08-CCT-1999; 07-CCT-1999; 08-CCT-1999; 08-CCT-1999; 08-CCT-1999; 13-AUG-1999; 13-AUG-1999; 13-AUG-1999; 14-CCT-1999; 15-CCT-1999; 16-CCT-1999; 17-CCT-1999; 18-CCT-1999; 18-CCT-1999; 19-CCT-1999; 19

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28-OCT-1999;
28-OCT-1999;
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 25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
                                                                                                                                                                 Protein identification; signal hybridisation assay; genetic matermination sequence.
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                                                                                                                                       Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                                             standard; Protein;
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PR 07-OCT-1999; 99US-0158029. PR 12-OCT-1999; 99US-0158232. PR 11-OCT-1999; 99US-0158286. PR 12-OCT-1999; 99US-0158293. PR 13-OCT-1999; 99US-0152294. PR 13-OCT-1999; 99US-0152294. PR 14-OCT-1999; 99US-0153239. PR 14-OCT-1999; 99US-0159331. PR 14-OCT-1999; 99US-0159331. PR 14-OCT-1999; 99US-0156331. PR 21-OCT-1999; 99US-016631. PR 21-OCT-1999; 99US-0160741. PR 21-OCT-1999; 99US-0160768. PR 21-OCT-1999; 99US-0160141. PR 21-OCT-1999; 99US-016014. PR 22-OCT-1999; 99US-016014. PR 22-OCT-1999; 99US-0161404. PR 22-OCT-1999; 99US-0161406. PR 25-OCT-1999; 99US-0161406. PR 25-OCT-1999; 99US-0161361. PR 26-OCT-1999; 99US-0161361. PR 26-OCT-1999; 99US-0161361. PR 28-OCT-1999; 99US-0161361.	Query Match Best Local Similarity 32.1%; Pred. No. 1.1e-40; Bast Local Similarity 32.1%; Pred. No. 1.1e-40; Matches 164; Conservative 73; Mismatches 175; Indels 99; Ga Qy 3 GASTPQTLYDKVLQAHVVDEKLDGTVLLYIDRHLVHEVTSPQAFEGLRNAGRKV Db 6: GSTVTCMMMTRT:	58 RRPDCTLATTDHNVPTTSRKALKDIASFIKEDDSRTQCVTLEENVKEF 119 KWMDPEKIVVIPDHYIFTADKRANNNVDIMREHCREQNIKYPYD 112 LSDKRQGIVVIGPEQGFTLPGTTVVGDSHTSTHGAFGALAFGIGTSEVEH 113 IN 1	QY 172 TKRSKNMRIQVDGELAPGVSSKDVVLHAIGIIGTAGGTGAVIEFCGSVIRSLSMEARMSI	QY 289 IDVFIDAKDIVPTLIMGTSPEDVVPITGVVPDPETFATEAKKADGRRMLQYMGLKAGTPM Db 335 ADYRFDVSKLEPVVAKPHSPDNRALARECK	95 (24 (76 I
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Matches 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plan with nucleic acid or amino acid sequences from non-plant organisms us suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypoptides or nucleic acids encoding the are useful for identifying modulators. The identified modulators are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
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IDVFIDAKDIVPTLTWGTSPEDVVPITGVVPDPETFATEAKKADGRRMLQYMGLKAGTPM 348
                                                                                                                                                             LKVPPTMRFILDGEMPSYLQAKDLILQIIGEISVAGATYKTMEFSGTTIESLSMEERMTL
                                                                                                                                                                                                 TKRSKNMRIQVDGELAPGVSSKDVVLHAIGIIGTAGGTGAVIEFCGSVIRSLSMEARMSI
                                                                                                                                                                                                                                                                     ANPDYKGVCHVALAQEGHCRPGEVLLGTDSHTCTAGAFGQFATGIGNTDAGFVLGTGKIL
                                                                                                                                                                                                                                                                                                                  LSDKRQGIVHVIGPEQGFTLPGTTVVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLI
                                                                                                                                                                                                                                                                                                                                                                                                                                  R--RPDCTLATTDHNVPTTSRKALKDIASFIKEDDSRTQCVTLEENVKEF----GVTYFG
                                                        CNMVVEAGGKNGVIPPDATTLNYVEACILSCFLPVY-------
                                                                                                       CNMSIEGGARAGMVAPDEITFEYLKGRPLA---PKYDSPEWHKATQYWKNLQSDPGAKYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             509
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21-MAY-1999;
24-MAY-1999;
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27-MAY-1999;
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06-MAY-1999;
07-MAY-1999;
11-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                            Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control;
                                                                                                                                                                                                                                                 01-APR-1999;
06-APR-1999;
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05-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana.
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                                                                                                                                                  04-MAY-1999;
05-MAY-1999;
                                                                                                                                                                    30-APR-1999;
30-APR-1999;
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23-APR-1999;
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                                                                                                                                                                                                                                         08-APR-1999;
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25-MAR-1999;
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                                                                     14-MAY-1999;
18-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADYRFDVSKLEPVV---AKPHS-----PDNRALARECK---
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                                                                                                                                                                                                                                                                                                                                                                                                    sequence
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                                                                                                                                                                                                                                                                                                                                2000EP-0301439
99US-0136392.
99US-0136782.
99US-0137222.
                        99US-0134768.
99US-0134941.
99US-0135124.
99US-0135353.
99US-0135629.
99US-0136021.
                                                                             99US-0132863.
99US-0134256.
99US-0134218.
99US-0134219.
99US-0134221.
99US-0134370.
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99US-0132407.
99US-0132484.
99US-0132485.
99US-0132486.
99US-0132487.
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99US-0130510.
99US-0130891.
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promoter;
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06 - AUG-1999999999999999999999999999999999999	Query Match
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25 FEB-1999

05-MAR-1999

09-WAR-1999

23-MAR-1999

23-MAR-1999

29-MAR-1999

01-APR-1999

06-APR-1999

16-APR-1999

16-APR-1999

19-APR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TKRSKNMRIQVDGELAPGVSSKDVVLHAIGIIGTAGGTGAVIEFCGSVIRSLSMEARMSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; Protein;
                                                                                                                                                                                                                               2000EP-0301439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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99US-0123180
99US-0123548
99US-0125788
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2; Mismatches 176;
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expression control;
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promoter;
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     08-JUN-1999;
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17-JUN-1999;
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PR 20-JUL-1999; 99US-0144814.

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PR 21-JUL-1999; 99US-0144814.

PR 22-JUL-1999; 99US-0144814.

PR 22-JUL-1999; 99US-0144086.

PR 22-JUL-1999; 99US-0145086.

PR 22-JUL-1999; 99US-0145086.

PR 22-JUL-1999; 99US-0145086.

PR 22-JUL-1999; 99US-0145086.

PR 23-JUL-1999; 99US-0145087.

PR 22-JUL-1999; 99US-0145089.

PR 22-JUL-1999; 99US-0147129.

PR 02-AUG-1999; 99US-0147129.

PR 02-AUG-1999; 99US-0147139.

PR 12-AUG-1999; 99US-0147139.

PR 12-AUG-1999; 99US-0149310.

PR 13-AUG-1999; 99US-0149310.

PR 13-AUG-1999; 99US-0149310.

PR 13-AUG-1999; 99US-0149310.

PR 13-AUG-1999; 99US-0149310.

PR 22-AUG-1999; 99US-0149310.

PR 23-AUG-1999; 99US-015303.

PR 24-AUG-1999; 99US-015303.

PR 24-AUG-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SKLEPVV---AKPHS------PDNRALARECK-------DVKIDR 304
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                                                                                                                                                                                                                                                                                                                                                                       63 TLATTDHNVPTTSRKALKDIASFIKEDDSRTQCVTLEENVKEF----GVTYFGLSDKRQG 118
                                                                                                                                                                                                                                                                                                                                                                                                                   IVHVIGPEQGFTLPGTTVVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNM 178
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                           62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :: | :: | :: | :: | :: | :: | IVVIPDHYIFTADKRANRNV-----DIMREHC--REQNIKYFYDITDLGNFKANPDYKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GARAGMVAPDEITFEYLKGRPLA---PKYDSPEWHKATQYWKNLQSDPGAKYDIDVFIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLYDKVLQAHVVDEKL---DGTVLLYIDRHLVHEVTSPQAFEGL--RNAGRKVR--RPDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VFIGSCTNSRIEDLRAAAAV--VKGRK-KAPNV------KSAMVVPGSGLVKTQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EBEGLDKIFEBAGFEW-REAGCSMCLGMNPDILA----PQERCASTSNRNFEGROG-AGG
                                                                                                                                                                                                                                                                              Length 443;
                                                                                                                                                                                                                                                                             13.6%; Score 550.5; DB 21; Length 32.1%; Pred. No. 4.6e-40; ive 72; Mismatches 171; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG40227 standard; Protein; 451 AA
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QIYLASPYTAAASALTGRVADPRE 440
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         990S-0159637-
990S-0159638-
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990S-0160761-
990S-0160767-
990S-0160767-
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Matches 162; Conservative
14-0CT-1999;
14-0CT-1999;
18-0CT-1999;
21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
26-0CT-1999;
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AAG40227
ID AAG40
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DT 18-OC
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signal transduction pathway; metabolic pathway; enetic mapping; gene expression control; promoter; 21825 2186 22186 22187 221	rocein fragment SEO ID NO: 4984. PR 23-UNN-1999 10:4399			05-MAY-1999; 99) 06-MAY-1999; 99) 06-MAY-1999; 99) 07-MAY-1999; 99) 11-MAY-1999; 99) 11-MAY-1999; 99) 14-MAY-1999; 99) 14-MAY-1999; 99) 14-MAY-1999; 99) 14-MAY-1999; 99) 14-MAY-1999; 99) 15-MAY-1999; 99) 21-MAY-1999; 99) 21-MAY-1999; 99)		
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Bscherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to obtain antibodies capable of binding to the expressed proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carr GJ;
                               306
                                                             393
                                                                                                                                                    416
DIDVFIDAKDIVPTLTWGTSPEDVVPITGVVPDPETFATEAKKADGRRMLQYMGLKAGTP 347
                                                                             394 SGLVKTQAEEEGLDKIFEEAGFEW-REAGCSMCLGMNPDILA----PQERCASTSNRNFE
                                                                                                                                        365 AG-GKTCAQ-----IFEEAGCDTPASPSCGACLGGPADTYARLNEFQV-CVSTTNRNFP
                                                             ---KSAMVVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                 eseudomonas aeruginosa cellular proliferation protein #297.
                                                                                                                                                                                                                                                                                                                                                                                                             Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                               MEDIPVDKVFIGSCTNSRIEDLRAAAAV--VKGRK-KAPNV--
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                                 VADYRFDVSKLEPVV---AKPHS------PDNRALARECK
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                                                                                                                                                                                                    449 GRQG-AGGRTHLMSPVMAAAAGIVGKLADVRK 479
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2000US-207727F.
2000US-242578F.
2000US-253625F.
2000US-25731F.
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26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 IVHVIGPEQGFTLPGTTVVCGDSHTSTHGAFGALAFGIGTSEVEHVLATQCLITKRSKNM 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIQVDGELAPGVSSKDVVLHAIGIIGTAGGTGAVIEFCGSVIRSLSMEARMSICNMSIEG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 TLATTDHNVPITSRKALKDIASFIKEDDSRTQCVTLEENVKEF----GVTYFGLSDKRQG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 IVVIPDHYIFTADKRANRNV-----DIMREHC--REQNIKKFYDITDLGNFKANPDYKG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 TLYDKVLQAHVVDEKL---DGTVLLYIDRHLVHEVTSPQAFEGL--RNAGRKVR--RPDC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.6%; Score 550.5; DB 21; Length 451; 31.6%; Pred. No. 4.7e-40; ive 71; Mismatches 172; Indels 107;
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990S-0161920.
990S-0161992.
990S-0161993.
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99US-0161405.
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99US-0153758.
99US-0154018.
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99US-0157753.
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99US-0160981.
99US-0160989.
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99US-0155486.
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99US-0156458.
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              99US-0151303
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25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
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28-0CT-1999;
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13-0CT-1999;
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18-0CT-1999;
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21-OCT-1999;
21-OCT-1999;
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22-SEP-1999;
23-SEP-1999;
24-SEP-1999;
28-SEP-1999;
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06-OCT-1999;
07-OCT-1999;
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Matches 162;
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                                                                                                                                                                                                                                                    Query Match 13.4%; Score 542; DB 22; Length 212; Best Local Similarity 53.3%; Pred. No. 8e-40; Matches 112; Conservative 34; Mismatches 50; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                               essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                            Sequence
                                            712 NGLDDIGLTMOMEDKIAEFEAKMTRETPWL 741
                                                                                             596 --DFVLNKEPYRKASILVCTGANFGCGSSREHAPWALNDFGIRSVIAPSFADIFFNNSFK 653
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